

11/11
H/1
MAY 07 2002 SEQUENCE LISTING

<110> Li, Jing
Powers, Scott
Xiang, Phil
Peng, Yue
Tularik Inc.

<120> PRC17: An Amplified Cancer Gene

<130> 018781-007610US

<140> US 10/071,838
<141> 2001-02-08

<150> US 60/267,615
<151> 2001-02-08

<160> 18

<170> PatentIn Ver. 2.1

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<213> Homo sapiens

<220>
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Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His
35 40 45
Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu
50 55 60
Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp
65 70 75 80
Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp
85 90 95
Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser
100 105 110
Val Leu Leu Asn Ile Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr
115 120 125
Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg
130 135 140
Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg
145 150 155 160
Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala
165 170 175
Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His
180 185 190
Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp
195 200 205
Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe
210 215 220

His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu
225 230 235 240

His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Asp Lys
245 250 255

Lys Asp Leu Cys Gly Gln Cys Ser Pro Leu Gly Cys Leu Ile Arg Ile
260 265 270

Leu Ile Asp Gly Ile Ser Leu Gly Leu Thr Leu Arg Leu Trp Asp Val
275 280 285

Tyr Leu Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr Arg Ile Ala
290 295 300

Phe Lys Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro
305 310 315 320

Trp Ala Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala Arg Asp Glu
325 330 335

Asp Thr Val Leu Lys His Leu Arg Ala Ser Met Lys Lys Leu Thr Arg
340 345 350

Lys Gln Gly Asp Leu Pro Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser
355 360 365

Ala Ser Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys
370 375 380

Gly Asp Arg Gln Ala Pro Pro Gly Pro Pro Ala Arg Phe Pro Arg Pro
385 390 395 400

Ile Trp Ser Ala Ser Pro Pro Arg Ala Pro Arg Ser Ser Thr Pro Cys
405 410 415

Pro Gly Gly Ala Val Arg Glu Asp Thr Tyr Pro Val Gly Thr Gln Gly
420 425 430

Val Pro Ser Pro Ala Leu Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg
435 440 445

Phe Leu Gln Trp Asn Ser Met Pro Arg Leu Pro Thr Asp Leu Asp Val
450 455 460

Glu Gly Pro Trp Phe Arg His Tyr Asp Phe Arg Gln Ser Cys Trp Val
465 470 475 480

Arg Ala Ile Ser Gln Glu Asp Gln Leu Ala Pro Cys Trp Gln Ala Glu
485 490 495

His Pro Ala Glu Arg Val Arg Ser Ala Phe Ala Ala Pro Ser Thr Asp
500 505 510

Ser Asp Gln Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln Pro Cys Ala
515 520 525

Pro Thr Ser Gly Pro Cys Leu Cys Gly Leu His Leu Glu Ser Ser Gln
530 535 540

Phe Pro Pro Gly Phe

545

<210> 3
<211> 2146
<212> DNA
<213> Homo sapiens

<220>
<223> human PRC17 splice variant 1 (exon 3 expanded)

<220>
<221> CDS
<222> (1)..(1832)

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<211> 610
<212> PRT
<213> Homo sapiens

<220>

<223> human PRC17 splice variant 1 (exon 3 expanded)

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20 25 30

Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His
35 40 45

Leu Gly Ile Val Gln Ser Cys Arg Ser Trp Glu Ser Ala Pro Gln Glu
50 55 60

Gly Pro Cys Pro Pro Phe Pro Val Pro Ser Pro Gly Leu Ser Pro Glu
65 70 75 80

Leu Glu Arg Asp Arg Ala Ser Pro Phe Trp Gly Ser Ala Pro Arg Leu
85 90 95

Gly Pro Leu Gln Ala Pro Cys Ser Ser Ser Ala Leu Pro Gly Leu Pro
100 105 110

Tyr Ser Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu Ala Lys Gln
115 120 125

Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp Met Leu Gly
130 135 140

Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp Arg Ala Tyr
145 150 155 160

Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser Val Leu Leu
165 170 175

Asn Ile Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr Gln Ile Met
180 185 190

Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg Ile Asp Arg
195 200 205

Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg Asp Arg Tyr
210 215 220

Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala Tyr Glu Glu
225 230 235 240

Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His Ile Ala Ala
245 250 255

Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp Ala Leu Val
260 265 270

Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe His Ser Pro
275 280 285

Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu His Val Val
290 295 300

Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Asp Lys Lys Asp Leu
305 310 315 320

Cys Gly Gln Cys Ser Pro Leu Gly Cys Leu Ile Arg Ile Leu Ile Asp
325 330 335

Gly Ile Ser Leu Gly Leu Thr Leu Arg Leu Trp Asp Val Tyr Leu Val
340 345 350

Glu Gly Glu Gln Ala Leu Met Pro Ile Thr Arg Ile Ala Phe Lys Val
355 360 365

Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro Trp Ala Arg
370 375 380

Phe Cys Asn Arg Phe Val Asp Thr Trp Ala Arg Asp Glu Asp Thr Val
385 390 395 400

Leu Lys His Leu Arg Ala Ser Met Lys Lys Leu Thr Arg Lys Gln Gly
405 410 415

Asp Leu Pro Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser Ala Ser Arg
420 425 430

Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys Gly Asp Arg
435 440 445

Gln Ala Pro Pro Gly Pro Pro Ala Arg Phe Pro Arg Pro Ile Trp Ser
450 455 460

Ala Ser Pro Pro Arg Ala Pro Arg Ser Ser Thr Pro Cys Pro Gly Gly
465 470 475 480

Ala Val Arg Glu Asp Thr Tyr Pro Val Gly Thr Gln Gly Val Pro Ser
485 490 495

Pro Ala Leu Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg Phe Leu Gln
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Trp Asn Ser Met Pro Arg Leu Pro Thr Asp Leu Asp Val Glu Gly Pro
515 520 525

Trp Phe Arg His Tyr Asp Phe Arg Gln Ser Cys Trp Val Arg Ala Ile
530 535 540

Ser Gln Glu Asp Gln Leu Ala Pro Cys Trp Gln Ala Glu His Pro Ala
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Glu Arg Val Arg Ser Ala Phe Ala Ala Pro Ser Thr Asp Ser Asp Gln
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Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln Pro Cys Ala Pro Thr Ser
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Gly Pro Cys Leu Cys Gly Leu His Leu Glu Ser Ser Gln Phe Pro Pro
595 600 605

Gly Phe
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<212> DNA
<213> Homo sapiens

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<223> human PRC17 splice variant 2 (exon 10 deleted)

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<222> (1)...(1538)

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<211> 515
<212> PRT
<213> Homo sapiens

<220>
<223> human PRC17 splice variant 2 (exon 10 deleted)

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20 25 30

Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His
35 40 45

Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu
50 55 60

Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp
65 70 75 80

Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp
85 90 95

Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser
100 105 110

Val Leu Leu Asn Ile Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr
115 120 125

Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg
130 135 140

Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg
145 150 155 160

Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala
165 170 175

Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His
180 185 190

Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp
195 200 205

Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe
210 215 220

His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu
225 230 235 240

His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Tyr Leu
245 250 255

Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr Arg Ile Ala Phe Lys
260 265 270

Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro Trp Ala
275 280 285

Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala Arg Asp Glu Asp Thr
290 295 300

Val Leu Lys His Leu Arg Ala Ser Met Lys Lys Leu Thr Arg Lys Gln
305 310 315 320

Gly Asp Leu Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser Ala Ser
325 330 335

Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys Gly Asp
340 345 350

Arg Gln Ala Pro Pro Gly Pro Pro Ala Arg Phe Pro Arg Pro Ile Trp
355 360 365
Ser Ala Ser Pro Pro Arg Ala Pro Arg Ser Ser Thr Pro Cys Pro Gly
370 375 380
Gly Ala Val Arg Glu Asp Thr Tyr Pro Val Gly Thr Gln Gly Val Pro
385 390 395 400
Ser Pro Ala Leu Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg Phe Leu
405 410 415
Gln Trp Asn Ser Met Pro Arg Leu Pro Thr Asp Leu Asp Val Glu Gly
420 425 430
Pro Trp Phe Arg His Tyr Asp Phe Arg Gln Ser Cys Trp Val Arg Ala
435 440 445
Ile Ser Gln Glu Asp Gln Leu Ala Pro Cys Trp Gln Ala Glu His Pro
450 455 460
Ala Glu Arg Val Arg Ser Ala Phe Ala Ala Pro Ser Thr Asp Ser Asp
465 470 475 480
Gln Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln Pro Cys Ala Pro Thr
485 490 495
Ser Gly Pro Cys Leu Cys Gly Leu His Leu Glu Ser Ser Gln Phe Pro
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Pro Gly Phe
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<210> 7
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:forward primer
for PCR amplification of PRC17 cDNA

<400> 7
ggagggaaact gagaactttc ca 22

<210> 8
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:reverse primer
for PCR amplification of PRC17 cDNA

<400> 8
cgaacagcag tatgctccca c 21

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fluorescent-labeled PCR TaqMan detection probe for PRC17

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<221> modified_base
<222> (1)
<223> n = Fam-labeled t

<220>
<221> modified_base
<222> (20)
<223> n = TAMRA-labeled g

<400> 9
ncagggcctt gcctctgcgn

20

<210> 10
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:forward primer for full-length PRC17 splice variant 1 cDNA isolation

<400> 10
ggatatggca cggaccca

18

<210> 11
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:reverse primer for full-length PRC17 splice variant 1 cDNA isolation

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ggacctggac gtagagggc

19

<210> 12
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR TaqMan detection probe for PRC17 splice variant 1

<220>
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<222> (1)
<223> n = Fam-labeled t

<220>
<221> modified_base
<222> (29)
<223> n = TAMRA-labeled a

<400> 12
nctgtctgaa atcataatgg cggaaccan

<210> 13
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:6-His epitope tag

<400> 13
His His His His His His
1 5

<210> 14
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:anti-DYKDDDDK epitope tag

<400> 14
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 15
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:poly-Gly flexible linker

<220>
<221> MOD_RES
<222> (6)..(200)
<223> Gly at positions 6-200 may be present or absent

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Gly
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Gly
20 25 30

Gly
35 40 45

Gly
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Gly
65 70 75 80

Gly
85 90 95

Gly
100 105 110

Gly
115 120 125

Gly
130 135 140

Gly
145 150 155 160

Gly
165 170 175

Gly
180 185 190

Gly Gly Gly Gly Gly Gly Gly
195 200

<210> 16
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:unique PRC17
C-terminal peptide

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Pro Ser Thr Ser Asp Gln Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln
1 5 10 15

Pro Cys

<210> 17
<211> 786
<212> PRT
<213> Homo sapiens

<220>
<223> human TRE-2/USP6

<400> 17

Met Asp Met Val Glu Asn Ala Asp Ser Leu Gln Ala Gln Glu Arg Lys
1 5 10 15

Asp Ile Leu Met Lys Tyr Asp Lys Gly His Arg Ala Gly Leu Pro Glu
20 25 30

Asp Lys Gly Pro Glu Pro Val Gly Ile Asn Ser Ser Ile Asp Arg Phe
35 40 45

Gly Ile Leu His Glu Thr Glu Leu Pro Pro Val Thr Ala Arg Glu Ala
50 55 60

Lys Lys Ile Arg Arg Glu Met Thr Arg Thr Ser Lys Trp Met Glu Met
65 70 75 80

Leu Gly Glu Trp Glu Thr Tyr Lys His Ser Ser Lys Leu Ile Asp Arg
85 90 95

Val Tyr Lys Gly Ile Pro Met Asn Ile Arg Gly Pro Val Trp Ser Val
100 105 110

Leu Leu Asn Ile Gln Glu Ile Lys Leu Lys Asn Pro Gly Arg Tyr Gln
115 120 125

Ile Met Lys Glu Arg Gly Lys Arg Ser Ser Glu His Ile His His Ile
130 135 140

Asp Leu Asp Val Arg Thr Thr Leu Arg Asn His Val Phe Phe Arg Asp
145 150 155 160

Arg Tyr Gly Ala Lys Gln Arg Glu Leu Phe Tyr Ile Leu Leu Ala Tyr
165 170 175

Ser Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His Ile
180 185 190

Thr Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp Ala
195 200 205

Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Pro Gly Phe His
210 215 220

Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu His
225 230 235 240

Val Val Pro Lys Ser Gln Pro Lys Thr Met Trp His Gln Asp Lys Glu
245 250 255

Gly Leu Cys Gly Gln Cys Ala Ser Leu Gly Cys Leu Leu Arg Asn Leu
260 265 270

Ile Asp Gly Ile Ser Leu Gly Leu Thr Leu Arg Leu Trp Asp Val Tyr
275 280 285

Leu Val Glu Gly Glu Gln Val Leu Met Pro Ile Thr Ser Ile Ala Leu
290 295 300

Lys Val Gln Gln Lys Arg Leu Met Lys Thr Ser Arg Cys Gly Leu Trp
305 310 315 320

Ala Arg Leu Arg Asn Gln Phe Phe Asp Thr Trp Ala Met Asn Asp Asp
325 330 335

Thr Val Leu Lys His Leu Arg Ala Ser Thr Lys Lys Leu Thr Arg Lys
340 345 350

Gln Gly Asp Leu Pro Pro Pro Ala Lys Arg Glu Gln Gly Ser Leu Ala
355 360 365

Pro Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys Gly
370 375 380

Tyr Arg Gln Ala Pro Pro Gly Pro Pro Ala Gln Phe Gln Arg Pro Ile
385 390 395 400

Cys Ser Ala Ser Pro Pro Trp Ala Ser Arg Phe Ser Thr Pro Cys Pro
405 410 415

Gly Gly Ala Val Arg Glu Asp Thr Tyr Pro Val Gly Thr Gln Gly Val
420 425 430

Pro Ser Leu Ala Leu Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg Phe
435 440 445

Leu Glu Trp Lys Ser Met Pro Arg Leu Pro Thr Asp Leu Asp Ile Gly
450 455 460

Gly Pro Trp Phe Pro His Tyr Asp Phe Glu Arg Ser Cys Trp Val Arg
465 470 475 480

Ala Ile Ser Gln Glu Asp Gln Leu Ala Thr Cys Trp Gln Ala Glu His
485 490 495

Cys Gly Glu Val His Asn Lys Asp Met Ser Trp Pro Glu Glu Met Ser
500 505 510

Phe Thr Ala Asn Ser Ser Lys Ile Asp Arg Gln Lys Val Pro Thr Glu
515 520 525

Lys Gly Ala Thr Gly Leu Ser Asn Leu Gly Asn Thr Cys Phe Met Asn
530 535 540

Ser Ser Ile Gln Cys Val Ser Asn Thr Gln Pro Leu Thr Gln Tyr Phe
545 550 555 560

Ile Ser Gly Arg His Leu Tyr Glu Leu Asn Arg Thr Asn Pro Ile Gly
565 570 575

Met Lys Gly His Met Ala Lys Cys Tyr Gly Asp Leu Val Gln Glu Leu
580 585 590

Trp Ser Gly Thr Gln Lys Ser Val Ala Pro Leu Lys Leu Arg Arg Thr
595 600 605

Ile Ala Lys Tyr Ala Pro Lys Phe Asp Gly Phe Gln Gln Asp Ser
610 615 620

Gln Glu Leu Leu Ala Phe Leu Leu Asp Gly Leu His Glu Asp Leu Asn
625 630 635 640

Arg Val His Glu Lys Pro Tyr Val Glu Leu Lys Asp Ser Asp Gly Arg
645 650 655

Pro Asp Trp Glu Val Ala Ala Glu Ala Trp Asp Asn His Leu Arg Arg
660 665 670

Asn Arg Ser Ile Ile Val Asp Leu Phe His Gly Gln Leu Arg Ser Gln
675 680 685

Val Lys Cys Lys Thr Cys Gly His Ile Ser Val Arg Phe Asp Pro Phe
690 695 700

Asn Phe Leu Ser Leu Pro Leu Pro Met Asp Ser Tyr Met Asp Leu Glu
705 710 715 720

Ile Thr Val Ile Lys Leu Asp Gly Thr Thr Pro Val Arg Tyr Gly Leu
725 730 735

Arg Leu Asn Met Asp Glu Lys Tyr Thr Gly Leu Lys Lys Gln Leu Arg
740 745 750

Asp Leu Cys Gly Leu Asn Ser Glu Gln Ile Leu Leu Ala Glu Val His
755 760 765

Asp Ser Asn Ile Lys Ile Ser Pro Leu His His Leu Gln Met Glu Cys
770 775 780

Ser Pro
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<212> PRT

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<220>

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<400> 18

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Asp Ile Ile Met Lys Tyr Glu Lys Gly His Arg Ala Gly Leu Pro Glu
20 25 30

Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His
35 40 45

Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu
50 55 60

Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp
65 70 75 80

Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp
85 90 95

Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser
100 105 110

Val Leu Leu Asn Ile Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr
115 120 125

Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg
130 135 140

Ile Asp Arg Asp Ile Ser Gly Thr Leu Arg Lys His Met Phe Phe Arg
145 150 155 160

Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala
165 170 175

Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His
180 185 190

Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp
195 200 205

Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe
210 215 220

His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu
225 230 235 240

His Val Val Ala Thr Ser Gln Ser Lys Thr Met Gly His Gln Asp Lys
245 250 255

Lys Asp Leu Cys Gly Gln Cys Ser Pro Leu Gly Cys Leu Ile Arg Ile
260 265 270

Leu Ile Asp Gly Ile Ser Leu Gly Leu Thr Leu Arg Leu Trp Asp Val
275 280 285

Tyr Leu Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr Arg Ile Ala
290 295 300

Phe Lys Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro
305 310 315 320

Trp Ala Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala Arg Asp Glu
325 330 335

Asp Thr Val Leu Lys His Leu Arg Ala Ser Met Lys Lys Leu Thr Arg
340 345 350

Lys Gln Gly Asp Leu Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser
355 360 365

Ala Ser Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys
370 375 380

Gly Asp Arg Gln Ala Pro Pro Gly Pro Pro Ala Arg Phe Pro Arg Pro
385 390 395 400

Ile Trp Ser Ala Ser Pro Pro Arg Ala Pro Arg Ser Ser Thr Pro Cys
405 410 415

Pro Gly Gly Ala Val Arg Glu Asp Thr Tyr Pro Val Gly Thr Gln Gly
420 425 430

Val Pro Ser Pro Ala Leu Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg
435 440 445

Phe Leu Gln Trp Asn Ser Met Pro Arg Leu Pro Thr Asp Leu Asp Val
450 455 460

Glu Gly Pro Trp Phe Arg His Tyr Asp Phe Arg Gln Ser Cys Trp Val
465 470 475 480

Arg Ala Ile Ser Gln Glu Asp Gln Leu Ala Pro Cys Trp Gln Ala Glu
485 490 495

His Pro Ala Glu Arg Val Arg Ser Ala Phe Ala Ala Pro Ser Thr Asp
500 505 510

Ser Asp Gln Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln Gln Tyr Ala
515 520 525

Pro Thr Ser Gly Pro Cys Leu Cys Gly Leu His Leu Glu Ser Ser Gln
530 535 540

A1
Phe Pro Pro Gly Phe
545